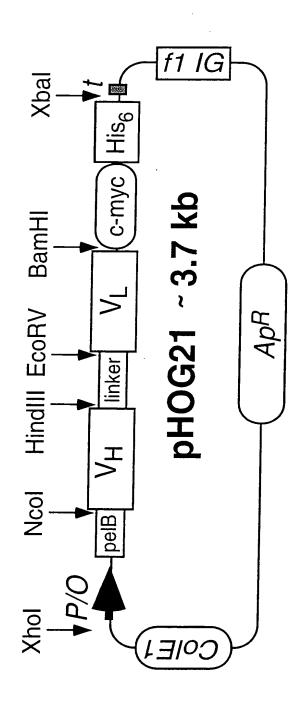
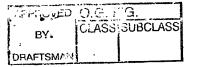
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TOPP VOM ES STENCE :

EcoRI RBS PelB leader
131 GAATTCATTAAAGAGGAGAAATTAACCATGAAATACCTATTGCCTACGGCAGCCGCTGGCT
1 M K Y L L P T A A A G
Pstl
Ncol ♦ Pvull VH anti-CD3
192 TGCTGCTGCAGCTCAGCCGGCCATGGCGCAGGTGCAGCTGCAGCAGTCTGGGGCTGAA 12 L L L A A Q P A M A Q V Q L Q Q S G A F
12 L L L A A Q P A M A Q V Q L Q Q S G A E Frame-H1
254 CTGGCAAGACCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTACT <u>A G</u>
33 LARPGAS VKMSCKASG YTFTR
CDR-H1 Frame-H2
316 GTACACGATGCACTGGGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGATACA
53 Y T M H W V K Q R P G Q G L E W I G Y
CDR-H2
375 TTAATCCTAGCCGTGGTTATACTAATTACAATCAGAAGTTCAAGGACAAGGCCA
73 I N P S R G Y T N Y N Q K F K D K A
Frame-H3
429 CATTGACTACAGACAAATCCTCCAGCACAGCCTACATGCAACTGAGCAGCCTGACATCTGAG 91 T L T T D K S S S T A Y M O L S S L T S E
Psti CDR-H3 491 GACTCTGCAGTCTATTACTGTGCAAGA <u>TATTATGATGATCATTACAGCCTTGACTAC</u>
112 D S A V Y Y C A R Y Y D D H Y S L D Y
Frame-H4 CH1 HindIII Yol linker
548 TGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAAAACAACACCCAAGCTTGAAGAAGG
131 W G Q G T T L T V S S A K T T P K L E E G
E∞RV
Mlul VL anti-CD3 Frame-L1
Mlul VL anti-CD3 Frame-L1 610 <u>TGAATTTTCAGAAGCACGC</u> GTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT
Mlu! VL anti-CD3 Frame-L1 610 <u>TGAATTTTCAGAAGCACGC</u> GTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151▶ E F S E A R V D I V L T Q S P A I M S A
Mlu! VL anti-CD3 Frame-L1 610 <u>TGAATTTTCAGAAGCACGC</u> GTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151▶ E F S E A R V D I V L T Q S P A I M S A Pst! CDR-L1
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA
Mlu! VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pst! CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M
Mlu! VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pst! CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCAAAAGATGGATTTATGACACATCCAAA
Mlu! VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pst! CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3
Mlu! VL anti-CD3 Frame-L1 610 TGAATTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pst! CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCTGCTCACTTCAGGGGGCAGTGGGTCTGGGACCTCTCTCT
Mlu! VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pst! CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCCTGCTCACTTCAGGGGCAGTGGGTCTGGGACCTCTTACTCTCTC 211 L A S G V P A H F R G S G S G T S Y S L
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGGAGTCCCTGCTCACTTCAGGGGCAGTGGGTCTGGGACCTCTTACTCTCTC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3
MIUI VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A PStI CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCCTGCTCACTTCAGGGGCAGTGGGTCTGGGACCTCTTACTCTCC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3 848 ACAATCAGCGGCATGGAGGCTGAAGATGCTTACTCCCCAGCAGTGGAGTAGGAGTAG
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCCTGCTCACTTCAGGGGGCAGTGGGTCTGGGACCTCTTACTCTCTC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3 848 ACAATCAGCGGCATGGAGGCTGAAGATGCTGCCACTTATTACTCCCCCCAGCAGTGGAGTAG 231 T I S G M E A E D A A T Y Y C Q Q W S S
Mlul VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCCTCACTTCAGGGGGCAGTGGGTCTGGGACCTCTTACTCTCTC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3 848 ACAATCAGCGGCATGGAGGCTGAAGATGCTGCCACTTATTACTGCCCAGCAGTGGAGTAG 231 T I S G M E A E D A A T Y Y C Q Q W S S Frame-L4 C kappa
Mlu! VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pst! CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCAGGTGCAGGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGGAGAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCCTGCTCACTTCAGGGGCAGTGGGTCTGGGACCTCTCTCCC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3 848 ACAATCAGCGGCATGGAGGTCAGAGATGCTGCCACTTATTACTCCCCAGGAGTGGATTACTCTCTC 231 T I S G M E A E D A A T Y Y C Q Q W S S Frame-L4 C kappa 907 TAACCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAACCGGGCTGATACTCCACC
Mill VL anti-CD3
Mlu! VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pst! CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCAGGTGCAGGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGGAGAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCCTGCTCACTTCAGGGGCAGTGGGTCTGGGACCTCTCTCCC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3 848 ACAATCAGCGGCATGGAGGTCAGAGATGCTGCCACTTATTACTCCCCAGGAGTGGATTACTCTCTC 231 T I S G M E A E D A A T Y Y C Q Q W S S Frame-L4 C kappa 907 TAACCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAACCGGGCTGATACTCCACC
MIUI VL anti-CD3 Frame-L1 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGGTGTAAGTTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 CDR-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCAAAAGATGGATTTATGACACTCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCCTGCTCACTTCAGGGGCAGTGGGTCTGGGACCTCTTACTCTCTC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3 848 ACAATCAGCGGCATGGAGGCTGAAGATGCTGCCACTTATTACTGCCCAGCAGTAGATAG 231 T I S G M E A E D A A T Y Y C Q Q W S S Frame-L4 C kappa 907 TAACCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAACCGGGCTGATACTGCACC 250 N P F T F G S G T K L E I N R A D T A P BamHI c-myc epitope His6 tail
Mill VL anti-CD3 Frame-L1 610 TGAATTTTCAGAAGCACGCGTAGATATCGTGCTCACTCAGTCTCCAGCAATCATGTCTGCAT 151 E F S E A R V D I V L T Q S P A I M S A Pstl CDR-L1 672 CTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGA 172 S P G E K V T M T C S A S S S V S Y M Frame-L2 729 ACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAA 191 N W Y Q Q K S G T S P K R W I Y D T S K Frame-L3 788 CTGGCTTCTGGAGTCCCTGCTCACTTCAGGGGCAGTGGGTCTGGGACCTCTTACTCTCTC 211 L A S G V P A H F R G S G S G T S Y S L CDR-L3 848 ACAATCAGCGGCATGGAGGCTGAAGATGCTGCCACTTATTACTGCCCAGCAGTGGAGTAG 231 T I S G M E A E D A A T Y Y C Q Q W S S Frame-L4 C Kappa 907 TAACCCATTCACGTTCGGCTCGCGGCACAAAGTTGGAAATAAACCGGGCTGATACTCCACC 250 N P F T F G S G T K L E I N R A D T A P BamHI c-myc epitope His6 tail 967 AACTGGATCCGAACAAAACCTGATCTCTCAGAAGAAGACCTAAACTCACCATC 270 T G S E Q K L I S E E D L N S H H H H H H Xbal
Mill VL anti-CD3

·VB

ACT CONCEPTION 23 MOVE MAY

EcoRI **RBS** PelB leader 1 GAATTCATTAAAGAGAGAAATTAACCATGAAAATACCTATTGCCTACGGCAGCCGCTGGCTTGCTG 1 M K Y L L PTAAAGLL ◆ VH anti-CD3 Ncol Frame-H1 67 CTGCTGGCAGCTCAGCCGGCCATGGCGCAGGTGCAGCTGCAGCAGTCTGGGGGCTGAACTGGCAAGAC 14 LLAAQPAMAQVQLQQS GAELAR CDR-H1 134 CTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTACTAGGTACACGATGCA 36 P G À S V K M S C K A S G Y T Y Frame-H2 CDR-H2 198 CTGGGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGATAAATCCTAGCCGTGG 57▶ W ·V K Q R P G Q G L E W I G Y Ν Frame-H3 261 TTATACTAATTACAATCAGAAGTTCAAGGACAAGGCCACATTGACTACAGACAAATCCTCCA N Y N Q K F K D K A T L T T D K S S 323 GCACAGCCTACATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA<u>T</u>A 99 S T A Y M Q 1\ S S L T S E D S A V Y Y C A R CDR-H3 Frame-H4 390 TTATGATGATCATTACAGCCTTGACTACTGGGGCCCAAGGCACCACTCTCACAGTCTCCTCAG S \L D Y WGQGTTLTVSS CH1 VL anti-CD19 Linker 452 CCAAAACACACCCAAGCTTGGCGGTGATATCTTGCTCACCCAAACTCCAGCTTCTTTGGCTGTG DILLTQT K L G Ġ PASLAV CDR-L1 164 S L G Q R A T I S C \ K A S Q S V D Y Frame-L2 579 TAGTTATTTGAACTGGTACCAACAGATTCCAGGACAGCCACCCAAACTCCTCATCTATGATGCA 184▶ S Y N W Y Q Q I P G O P P K L L I CDR-L2 Frame-L3 643 TCCAATCTAGTTTCTGGGATCCCACCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCACCC 206 S N V S G I P P R F S G S G T D F T L CDR-L3 707 TCAACATCCATCCTGTGGAGAAGGTGGATGCTGCAACCTAYCACTGTCAGCAAAGTACTGAGGA 227 L N I H P V E K V D A A T Y H C Q S Frame-L4 C kappa Noti 771 <u>T</u>CCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA<u>CGGGCTGATGCT</u>GCGGCCGCTGGATCC 248▶ PWTFGGGTKL E I K D A A A A G S c-myc epitope His6 tail BqIII 838 GAACAAAGCTGATCTCAGAAGAAGCCTAAACTCACATCACCATCACCATCACTAAAGAT 271▶ E Ι S E \mathbf{E} D L N S H H жннн 899 CT

Fig. 3

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Balll **RBS** Pel B leader 1 AGATCTATTAAAGAGGAGAAATTAACCATGAAATACCTATTGCCTACGGCAGCCGCTGGCTTGC 1 M K Y L L P Т VH anti-CD19 Frame-H1 TGCTGCTGGCAGCTCAGCCGGCCATGGCGCAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCTGGT L A A Q PAMAQVQLQ 0 SGAELV CDR-H1 129 GAGGCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTACTG R PG S S V K I S C K A S G Y A F Frame-H2 192 GATGAACIGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCT Ν V K Q R P G Q G L E W I G O ODR-H2 253 GGAGATGGTGÀTACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCA 76▶ G D G \mathbf{T} N Y N G K F KGKATLT Frame-H3 310 GACGAATCCTCCAGCAXAGCCTACATGCAACTCAGCAGCCTAGCATCTGAGGACTCTGCGGTCT S Т E S S AYMOLSSLASEDSAV CDR-H3 374 ATTTCTGTGCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACT 116 Y F C A R R E TTVGR Y Frame-H4 CH₁ Linker 431 <u>A.C</u>TGGGGTCAAGGAACCTCAGTCAGCGTCTCCTCAGCCAAAACAACACCCAAGCTTGGCGGT 135▶Y W G Q G T S V T\V S S A K T T P K VL anti-CD3 Frame-L1 493 GATATCGTGCTCACTCAGTCTCCAGCAAICATGTCTGCATCTCCAGGGGGAGAAGGTCACCATGA 156 DIVLTQSPAI\MSASPGE CDR-L1 Frame-L2 557 CCTGCAGTGCCAGCTCAAGTGTAAGTTACATGAACTGGTACCAGCAGAAGTCAGCCACC S V M N W Y O O K S G T S Y CDR-L2 616 TCCCCCAAAAGATGGATTTATGACACATCCAAA&TGGCTTCTGGAGTCCCTGCTCACTTC 197▶ S P K R W I Y K D T S Α SGVPAHF Frame-L3 676 AGGGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCGGCATGGAGGCTGAAGATGCTG 217 R G S G S G T S Y S L T I S G M E A E D A CDR-L3 740 CCACTTATTACTGCCAGCAGTGGAGTAGTAACCCATTCACGTTCGGCTCGGGGACAAAG 238▶A T Y Y C Q Q S S N Р F FGSGTK C kappa c-myc epitope 799 TTGGAAATAAACCGGGCTGATACTGCACCAACTGGATCCGAACAAAAGCTGATCTCAGAA TAPTGSE R A D Q VK. L His6 tail Xbal 859 GAAGACCTAAACTCACCATCACCATCACCATCACTAATCTAGA LNSHHHHH

Fig. 3 (Fortsetzung)